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Comparative analysis of the glycam-1 gene in camelids reveals conserved structure and genetic polymorphisms

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Abstract

In the context of global climate change, camelids are gaining attention for their adaptive traits and contributions to rural economies. Their relatively low selection pressure compared to other livestock makes them valuable models for exploring genetic diversity and identifying markers linked to economically important traits like milk production. In this study, we focused on the GlyCam⁻¹ gene, which encodes a whey glycoprotein involved in immune defense and associated with milk fat globules. The entire gene, along with its regulatory regions, was sequenced in both Old World (dromedary and bactrian) and New World Camelids (llama and alpaca) for a total of 3193/3120 bp, respectively. The gene structure was found to be conserved among the four species, with a slight difference in size (2,576 bp in OWC and 2,504 in NWC). Regulatory regions analysis revealed 119 common transcription factor binding sites (TFBS) among the four species, including factors related to milk and protein expression. Intraspecies sequence comparison showed that llamas and alpacas exhibited greater genetic diversity (32 and 40 polymorphic sites, respectively) compared to dromedary (21) and bactrian camels (7), while interspecies comparison revealed noteworthy SNPs in both regulatory and exonic regions. Two mutations g.163A>G and g.563C>T, found in the regulatory regions of NWC and dromedaries, respectively, disrupted MZF1 and NF- B TFBS, potentially affecting the immune response. Genotyping results revealed higher frequencies of the A (0.9) and T (0.77) alleles, respectively. In the exonic regions, two variants g.2324G>A and g.2823C>T resulted in amino acid substitutions (p.46Glu>Ser and p.136Ser>Pro), predicted to have deleterious effect on protein function. This study highlights the conservation of the GlyCam⁻¹ gene in camelids and its potential role in milk traits and immune function. Further investigation will clarify the impact of the found genetic diversity on Gly-Cam1 gene expression, and its potential use in future breeding programs.

Keywords: To add